

## ABSTRACT

### IDENTIFICATION OF BIOLOGICAL (MICRO)ORGANISMS BY DETECTION OF THEIR HOMOLOGOUS NUCLEOTIDE SEQUENCES ON ARRAYS

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The present invention is related to an identification and/or quantification method of a biological (micro)organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence 10 among at least 4 other homologous sequences and comprising the steps of:

- possibly extracting original nucleotide sequences (1) from the (micro)organism;
- amplifying or copying with a unique pair of primer(s), at 15 least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected;
- possibly labelling said target nucleotide sequences (2);
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide 20 sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, 25 quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3),  
wherein said capture nucleotide sequence (3) being bound to 30 the insoluble solid support (4) at a specific location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm<sup>2</sup> of solid support surface and

wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at the expected location, the detection of a single signal allowing a discrimination of the 5 target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences.

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